



# SEQUENCE LISTING

<110> Fisher F., Eric  
Edwards K., Carl  
Kieft L., Gary

<120> Truncated Soluble Tumor Necrosis Factor Type-I and  
Type-II Receptors

<130> 02-006

<140> 09/882,735

<141> 2001-06-15

<150> 09/214,613

<151> 1997-07-09

<150> PCT/US97/12244

<151> 1997-07-09

<150> 60/039,792

<151> 1997-03-04

<150> 60/039,314

<151> 1997-02-07

<150> 60/037,737

<151> 1997-01-23

<150> 60/032,534

<151> 1996-12-06

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<170> PatentIn Ver. 2.0

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<213> Homo sapiens

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<222> (1)..(483)

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1				5				10					15			

att	tgc	tgt	acc	aag	tgc	cac	aaa	gga	acc	tac	ttg	tac	aat	gac	tgt	96
Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	
			20					25					30			

cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144  
Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
35 40 45

ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192  
Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
50 55 60

tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240  
Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
65 70 75 80

cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288  
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95

agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336  
Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110

acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384  
Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125

cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432  
His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
130 135 140

tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480  
Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
145 150 155 160

aat 483  
Asn

<210> 2  
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<212> PRT  
<213> Homo sapiens

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Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys  
20 25 30

Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
35 40 45

Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
50 55 60

Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
65 70 75 80

Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
85 90 95

Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly  
100 105 110

Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys  
115 120 125

His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn  
130 135 140

Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu  
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Asn

<210> 3

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<213> Artificial Sequence

<220>

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2.6D/C105

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<222> (4)..(321)

<400> 3

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1 5 10 15

aat tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat 96  
Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn  
20 25 30

gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc 144  
Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser  
35 40 45

ggc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc 192  
Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys  
50 55 60

tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca 240  
Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr  
65 70 75

gtg gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat 288  
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His  
80 85 90 95

tat tgg agt gaa aac ctt ttc cag tgc ttc tgc tgataggatc c 332  
 Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys  
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           2.6D/C105

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           20                  25                  30  
 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
           35                  40                  45  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
           50                  55                  60  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
   65                  70                  75                  80  
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
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 Trp Ser Glu Asn Leu Phe Gln Cys Phe Cys  
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           2.6D/C106

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 <222> (4)..(330)

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   Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn  
   1                  5                  10                  15  
 aat tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat 96  
 Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn

	20	25	30	
gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc				144
Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser				
	35	40	45	
ggc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc				192
Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys				
	50	55	60	
tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca				240
Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr				
	65	70	75	
gtg gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat				288
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His				
	80	85	90	95
tat tgg agt gaa aac ctt ttc cag tgc ttc aat tgc tct ctg taaaagctt				339
Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu				
	100	105		

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<212> PRT

<213> Artificial Sequence

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2.6D/C106

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1 5 10 15

Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
20 25 30

Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
35 40 45

Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
50 55 60

Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val
65 70 75 80

Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr
85 90 95

Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu
100 105

<210> 7

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<220>  
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1 5 10 15  
  
aat tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat 96  
Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn  
20 25 30  
  
gac tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc 144  
Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser  
35 40 45  
  
ggc tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc 192  
Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys  
50 55 60  
  
tcc aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca 240  
Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr  
65 70 75  
  
gtg gac cgg gac acc gtg tgt ggt tgc agg aag aac cag tac cgg cat 288  
Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His  
80 85 90 95  
  
tat tgg agt gaa aac ctt ttc cag tgc ttc aat taatagggat cc 333  
Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn  
100 105

<210> 8  
<211> 106  
<212> PRT  
<213> Artificial Sequence

<220>  
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2.6D/N105

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Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp  
20 25 30

Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly  
           35                          40                          45  
 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser  
       50                              55                          60  
 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val  
       65                              70                          75                          80  
 Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr  
                           85                              90                          95  
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           100                              105

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 <213> Artificial Sequence

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       2.3D/d18

<220>  
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           1                              5                          10                          15  
 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 96  
       Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser  
                           20                              25                          30  
 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 144  
       Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys  
                           35                              40                          45  
 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 192  
       Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp  
           50                              55                          60  
 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 240  
       Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp  
           65                              70                          75  
 agt gaa aac ctt ttc cag tgc ttc aat tgc tct ctg taaaagctt 285  
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<212> PRT  
 <213> Artificial Sequence

<220>  
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 2.3D/d18

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 Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe  
                   20                  25                  30  
 Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys  
                   35                  40                  45  
 Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg  
           50                  55                  60  
 Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser  
           65                  70                  75                  80  
 Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu  
                   85                  90

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 2.3D/d8

<220>  
 <221> CDS  
 <222> (4)..(306)

<400> 11  
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       Met Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys  
           1                  5                  10                  15  
 cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat 96  
 His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp  
                   20                  25                  30  
 acg gac tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac 144  
 Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn  
                   35                  40                  45  
 cac ctc aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt 192  
 His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly  
           50                  55                  60



cag gtg gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc 240  
 Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly  
         65                        70                        75

tgc agg aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag 288  
 Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln  
         80                        85                        90                        95

tgc ttc aat tgc tct ctg taaaagctt 315  
 Cys Phe Asn Cys Ser Leu  
                         100

<210> 12  
 <211> 101  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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         2.3D/d8

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 Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr  
                 20                        25                        30  
 Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His  
         35                        40                        45  
 Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln  
         50                        55                        60  
 Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys  
         65                        70                        75                        80  
 Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys  
                 85                        90                        95  
 Phe Asn Cys Ser Leu  
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<400> 13

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1				5					10					15		

aat	gac	tgt	cca	ggc	ccg	ggg	cag	gat	acg	gac	tgc	agg	gag	tgt	gag	96
Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	
			20					25					30			

agc	ggc	tcc	ttc	acc	gct	tca	gaa	aac	cac	ctc	aga	cac	tgc	ctc	agc	144
Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	
		35						40					45			

tgc	tcc	aaa	tgc	cga	aag	gaa	atg	ggg	cag	gtg	gag	atc	tct	tct	tgc	192
Cys	Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	
		50					55					60				

aca	gtg	gac	cgg	gac	acc	gtg	tgt	ggc	tgc	agg	aag	aac	cag	tac	cgg	240
Thr	Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	
	65					70					75					

cat	tat	tgg	agt	gaa	aac	ctt	ttc	cag	tgc	ttc	aat	tgc	tct	ctg		285
His	Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu		
80					85					90						

taaaagctt																294
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: sTNFR-I  
2.3D/d15

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1				5					10					15	

Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	Cys	Arg	Glu	Cys	Glu	Ser
			20					25					30		

Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	Arg	His	Cys	Leu	Ser	Cys
		35						40				45			

Ser	Lys	Cys	Arg	Lys	Glu	Met	Gly	Gln	Val	Glu	Ile	Ser	Ser	Cys	Thr
	50					55					60				

Val	Asp	Arg	Asp	Thr	Val	Cys	Gly	Cys	Arg	Lys	Asn	Gln	Tyr	Arg	His
65					70					75					80

Tyr	Trp	Ser	Glu	Asn	Leu	Phe	Gln	Cys	Phe	Asn	Cys	Ser	Leu		
				85						90					

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 <212> DNA  
 <213> Homo sapiens

<220>  
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 <222> (1)..(705)

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 1 5 10 15

aca tgc cgg ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc 96  
 Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys  
 20 25 30

agc aag tgc tcg ccg ggc caa cat gca aaa gtc ttc tgt acc aag acc 144  
 Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr  
 35 40 45

tcg gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag ctc 192  
 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu  
 50 55 60

tgg aac tgg gtt ccc gag tgc ttg agc tgt ggc tcc cgc tgt agc tct 240  
 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser  
 65 70 75 80

gac cag gtg gaa act caa gcc tgc act cgg gaa cag aac cgc atc tgc 288  
 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys  
 85 90 95

acc tgc agg ccc ggc tgg tac tgc gcg ctg agc aag cag gag ggg tgc 336  
 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys  
 100 105 110

cgg ctg tgc gcg ccg ctg cgc aag tgc cgc ccg ggc ttc ggc gtg gcc 384  
 Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala  
 115 120 125

aga cca gga act gaa aca tca gac gtg gtg tgc aag ccc tgt gcc ccg 432  
 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro  
 130 135 140

ggg acg ttc tcc aac acg act tca tcc acg gat att tgc agg ccc cac 480  
 Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His  
 145 150 155 160

cag atc tgt aac gtg gtg gcc atc cct ggg aat gca agc agg gat gca 528  
 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala  
 165 170 175

gtc tgc acg tcc acg tcc ccc acc cgg agt atg gcc cca ggg gca gta 576  
 Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val

180	185	190	
cac tta ccc cag cca gtg tcc aca cga tcc caa cac acg cag cca act			624
His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr			
195	200	205	
cca gaa ccc agc act gct cca agc acc tcc ttc ctg ctc cca atg ggc			672
Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly			
210	215	220	
ccc agc ccc cca gct gaa ggg agc act ggc gac			705
Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp			
225	230	235	
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<212> PRT			
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Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys			
20	25	30	
Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr			
35	40	45	
Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu			
50	55	60	
Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser			
65	70	75	80
Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys			
85	90	95	
Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys			
100	105	110	
Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala			
115	120	125	
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro			
130	135	140	
Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His			
145	150	155	160
Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Arg Asp Ala			
165	170	175	
Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val			
180	185	190	

His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln His Thr Gln Pro Thr  
195 200 205

Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro Met Gly  
210 215 220

Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp  
225 230 235

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<210> 21  
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<210> 22  
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<210> 23  
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<210> 24  
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<220>  
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33